## STIC Biotechnology Systems Branch

## **CRF Problem Report**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):
Application Serial Number: $\frac{10/532,909}{10/13/2005}$ Filing Date: $\frac{10/33/2005}{10/13/2005}$ Date Processed by STIC: $\frac{10/33/2005}{10/33/2005}$
STIC Contact: Mark Spencer: Telephone: 571-272-2510; Fax: 571-273-0221
Nature of CRF Problem:
(circle one) Damaged or Unreadable (for Unreadable, see attached) Blank (no files on CRF) (see attached) Empty file (filename present, but no bytes in file) (see attached) Wrong file saved to CRF (invention title, docket number, or applicant(s) do not match those in official application) (see attached) Not saved in ASCII text Sequence Listing was embedded in the file. According to Sequence Rules,     submitted file should only be the Sequence Listing. Did not contain a Sequence Listing. (see attached sample) Other: Invalid Sequence Listing filed before cannot claim a prior application filed before
PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM TO REDUCE ERRORS.  SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm
1. EFS-Bio ( <a href="http://www.uspto.gov/ebc/efs/downloads/documents.htm">http://www.uspto.gov/ebc/efs/downloads/documents.htm</a> >, EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
<ol> <li>Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):</li> <li>U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,</li> </ol>

Revised 01/20/06

Alexandria, VA 22314

8/22/2003

Xin-Hua Feng and Yingxian Xiao

```
( Sample of Submitted file)
SEQUENCE LISTING
(1) GENERAL INFORMATION:
(iii) NUMBER OF SEQUENCES: 9
(2) INFORMATION FOR SEQ ID NO: 1:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 27 base pairs(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
                                            This is invalid
(D) TOPOLOGY: linear
(ii) MOLECULAR TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1
AACggatccaaaacgctgcctccgcga 27
(2) INFORMATION FOR SEQ ID NO: 2:(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
                                                Us applications which
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
                                                cannot claim a priol application filed befole
(ii) MOLECULAR TYPE: DNA
(iv) ANTI-SENSE: YES
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2
TAGACGCTGCAGGAGGCGCCTGGCT 25
(2) INFORMATION FOR SEQ ID NO: 3:
                                                 July 1st 1998 must be
en New Sequence Lules
format. This Sequence
toccaggatogtggg 60
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULAR TYPE: DNA
                                                                      listing es en bled sequence rules format.
See Sample Sequence listing attached for valid format.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3
ggatccaaaacgctgcctccgcgacagggcggaggacggagggcgtcccaggatcgtggg 60
ccetgggcetgacgcetcggagcactccetgctccgagcgggcccgatgtggtggaagct 120 CS LV
cgggagcgcggggagccgggggaaggccgcggggcagccgtcgggggtccccgatccgagcc 180
ccgcggccccgggctggcggtgtcggctgcaatccggcgggcacggccgggccgggctggg 240
ctcttggggcagccaggcgcctccttcag 269
(2) INFORMATION FOR SEQ ID NO: 4:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULAR TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4
AGAAGACGAagctaagcagggtcgggcctggttagtacttggatgggagaccgcctggga 60
ataccgggtgctgtaggctttttg 84
(2) INFORMATION FOR SEQ ID NO: 5:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULAR TYPE: DNA
(iv) ANTI-SENSE: YES
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5
TCGACAAAAAGCCTACAGCACCCGGTATTCCCAGGCGGTCTCCCATCCAAGTACTAACCA 60
GGCCCGACCCTGCTTAGCTTCGTCTTCT 88
(2) INFORMATION FOR SEQ ID NO: 6:
```

<sup>(</sup>i) SEQUENCE CHARACTERISTICS:

<sup>(</sup>A) LENGTH: 367 base pairs

<sup>(</sup>B) TYPE: nucleic acid

## Consult this

					•	
<110>	Smith, Joh	nn; Smithgen	e Inc.			
		-			-	
<120>	Example of	a Sequence	Listing		•	
-120-	01 00001				•	
<130>	01-00001			<i>:</i>		
<140>	PCT/EP98/0	0001				
<141>	1998-12-31		•			
	•			•		
<150>	US 08/999,					
<151>	1997-10-15		. *			
	•					•
<160>	4					
•				•		
<170>	PatentIn v	ersion 2.0				•
			•	-	•	
<210>	1					
<211> <212>	389					
<213>	DNA Paramecium	en				:
	r or omeer om	Sp.				
<220>						
<221>	CDS					•
<222>	(279)(38	39)				•
<300>						
<301>	Doe, Richar					
<302>	Isolation a	and Character	ization of a	Gene Encodir	ng a	
<303>	Journal of	com Parameciu	m sp.			
<304>	1	Genes				
<305>	4			•		
<306>	1-7				•	
<307>	1988-06-31					
<308>	123456 <sup>-</sup>					
<309>	1988-06-31			·		
-400s		,	•			
<400.> agctgtagtc	l artestatat					
agetytagte	attcctgtgt	cctcttctct	ctgggcttct	caccctgcta	atcagatete	60
agggagagtg	tcttgaccct	cctctgcctt	tgcagcttca	caggcaggca	ggcaggcagc	120
		-	- <del>-</del>		009	:
tgatgtggca	attgctggca	gtgccacagg	cttttcagcc	aggcttaggg	tgggttccgc	180
cgcggcgcgg	cggcccctct	cgcgctcctc	tegegeetet	ctctcgctct	cctctcgctc	240

```
gtt
 ggacctgatt aggtgagcag
                              gaggagggg
                                             cagttagc
                                                              atg
                                                                                atg
                                                                          tca
                                                                                      ttc
                                                                                            agc
                                                                                                   296
                                                              Met
                                                                    Val
                                                                          Ser
                                                                                Met
                                                                                      Phe
                                                                                            Ser
                                                                1
                                                                                        5
                                                                    gtt
ttg
      tct
             ttc
                  ·aaa
                         tgg
                               cct
                                     gga
                                            ttt
                                                  tgt
                                                       ttg
                                                              ttt
                                                                          tgt
                                                                                ttg
                                                                                      ttc
                                                                                            caa
                                                                                                   344
                                     Gly
 Leu
      Ser
             Phe
                   Lys
                         Trp
                               Pro
                                            Phe
                                                  Cys
                                                       Leu
                                                              Phe
                                                                    Val
                                                                          Cys
                                                                                Leu
                                                                                      Phe
                                                                                            Gln
                    10
                                                                                 20
                  gtc
Val
                                     tgt
                                                             ctg
                                                                    cag
      ccc
                                                       tca
tgt
             aaa
                         ctc
                               ccc
                                           cac
                                                  tca
                                                                          ccg
                                                                                aat
                                                                                      ctt
                                                                                                  389
      Pro
            Lys
                                           His
                                                                   Gln
Cys
                         Leu
                                     Cys
                                                 Ser
                                                       Ser
                                                             Leu
                                                                          Pro
                               Pro
                                                                                Asn
                                                                                      Leu
              25
                                             30
                                                                           35
<210>
               2
               37
<211>
<212>
               PRT
<213>
               Paramecium sp.
<400>
                                                             Trp
            Ser
                        Phe
Met
     Val
                  Met
                              Ser
                                     Leu
                                           Ser
                                                 Phe
                                                       Lys
                                                                   Pro
                                                                        Gly
                                                                                     Cys
                                                                                           Leu
                                                        10
                                                                                      15
      Val
                                                 Lys
25
Phe
            Cys
                  Leu
                        Phe
                              Gln
                                    Cys
                                                       Val
                                                             Leu
                                                                         Cys
                                                                               His
                                                                                     Ser
                                                                                           Ser
                                                                                30
            Pro
      Gln
Leu
                  Asn
                        Leu
<210>
              3
<211>
              11
<212>
              PRT
              Artificial Sequence
<213>
<220>
              Designed peptide based on size and polarity to act as a linker between the alpha and beta chains of Protein XYZ.
<223>
<400>
Met Val
                Leu Glu
           Asn
                              Pro
                                    Met
                                          His
                                                Thr
                                                      Glu
 1
<210>
<400>
000
```

table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	<b>M</b>
<120>	Title of Invention		М
<130>	File Reference	Personal file reference	M when filed prior to assignment of appl. number
<140>	Current Applica- tion Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOS	М
<170>	Software	Name of software used to create the Sequence Listing	Ο .
<210>	SEQ ID NO:#:	Response shall be an integer representing the SEQ ID NO shown	M -
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	м .

sequence mole- cule is DNA, RNA, or PRT (protein). If a nucleotide sequence con- tains both DNA and RNA frag- ments, the type shall be "DNA." In ad- dition, the combined DNA/ RNA molecule shall be further described in the <220 to <223> feature section. <pre> </pre> <pre> </pre> <pre> </pre> <pre> </pre> <pre> </pre> <pre> <pre> </pre> <pre> <pre> </pre> <pre> <pre> </pre> <pre> <pre> <pre></pre></pre></pre></pre></pre></pre>	<b>4212</b> 5	<b>M</b>		
cule is DNA, RNA, or PRT (protein). If a nucleotide sequence con- tains both DNA and RNA frag- ments, the type shall be "DNA." In ad- dition, the combined DNA/ RNA molecule shall be further described in the <220 to <223 feature section.	<212>	Туре	Whether presented sequence mole-	М
RNA, or FRT (protein). If a nucleotide sequence contains both DNA and RNA frag- ments, the type shall be "DNA." In ad- dition, the combined DNA/ RNA molecule shall be further described in the <220 to <223> feature section.  <223> feature section.  <220> Coganism Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence or granisms shall be further described in the <220 to <223> feature section.  <220> Feature  Leave blank after described in the <220> to <223> feature section.  <220> Feature  Leave blank after described in the sequence in in, " "Xaa," or a modified base was used in a sequence if in, " "Xaa," or a modified base was used in a sequence if in, " "Xaa," or a modified base was used in a sequence if in, " "Xaa," or a modified or unusual L-amino aid or under the fol- lowing conditions; if in, " "Xaa," or a modified base was used in a sequence if in, " "Xaa," or a modified or unusual L-amino aid or a modified base was used in a sequence if in, " "Xaa," or a modified base was used in a sequence if in, " "Xaa," or a modified base was used in a sequence if in, " "Xaa," or a modified base was used in a sequence if in, " "Xaa," or a modified base was used in a sequence if in the viting in the intervent			<del>-</del>	• •
(protein). If a nucleotide sequence con- tains both DNA and RNA frag- ments, the type shall be "DNA." In ad- dition, the combined DNA/ RNA molecule shall be further described in the <220> to <223> feature section.   C213> Organism Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Se- quence" organisms shall be further described in the <220> to <223> feature section.  C220> Feature Leave blank after capture section.  C220> Feature Section.  C220> C221-223> following conditions: if in, "," and ified or unusual leamino ased in a sequence; if ORGAN- ISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.  C221> Name/Key Provide appropriate identifier for lowing conditions: if "n," "Xaa," or ferably from a modified or unusual L-amino ST.25 (1998), Appendix 2, Tables 5 and 6  C222> Location Specify location within sequence; lowing conditions:				
sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section. <pre> </pre> <pre> </pre> <pre> </pre> <pre> </pre> <pre> </pre> <pre> <pre> </pre> <pre> </pre> <pre> </pre> <pre> <pre> <pre> <pre> </pre> <pre> <pre> <pre> <pre> <pre> </pre> <pre> <pre> <pre> <pre> <pre> <pre> <pre> <pre> </pre> <pre> <p< td=""><td></td><td></td><td></td><td>-</td></p<></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre>				-
tains both DNA and RNA frag- ments, the type shall be "DNA." In ad- dition, the combined DNA/ RNA molecule shall be further described in the <220 to <223> feature section.   C213> Organism Scientific name, i.e. Genus/species, Unknown or Artifi- cial Sequence. In addition, the "Unknown" or "Artificial Se- quence" organisms shall be further described in the <220 to <223> feature section.  C220> Feature Leave blank after <220 to <223> feature section.  C220> Feature Leave blank after <220 to <223> feature section.  C220> Feature Leave blank after <220 to <223> feature section.  C220> Feature Leave blank after <220 to <223> feature section.  C220> Feature Leave blank after c220 to <223> feature section.  C220> Feature Leave blank after c220 to <223> feature section.  C220> Feature Leave blank after c220 to <221> Seature section.  C220> Feature Leave blank after c220 to <221> Seature section.  C220> Feature Leave blank after c220 to <221> Seature section.  C220> Feature Leave blank after c220 to <221> Seature section.  C220> Feature Leave blank after c220 to <221> Seature section.  C220> Feature Leave blank after c220 to <221> Seature section.  C220> Feature Leave blank after c220 to <221> Seature section.  C220> Feature Leave blank after c220 to <221> Seature section.  M, under the following conditions: if "n," "Xaa," or modified base was used in a sequence section.  C220> Feature Scientific or will in sequence section.  M, under the following conditions: if "n," "Xaa," or modified or unusual L-amino section: Specify location will in sequence section.  C222> Location Specify location within sequence; lowing conditions:	•	•		
and RNA fragments, the type shall be "DNA." In addition, the combined DNA/ RNA molecule shall be further described in the <220 to <223 feature section.   Call Organism  Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220 to <2223 feature section.  Call Sequence organisms shall be further described in the call Sequence organisms shall be further described in the call Sequence organisms shall be further described in the call Sequence organisms shall be further described in the call Sequence organisms shall be further described in the call Sequence organisms shall be further described in the call Sequence organisms shall be further described in the call Sequence organisms shall be further described in the call Sequence organisms shall be further described in the call Sequence organisms shall be further described in the call Sequence if "n," "Xaa," or a modified base was used in a sequence; if "n," "Xaa," or "Ninknown"; if molecule is combined DNA/RNA.  Call Sequence organisms shall be further described in the call Sequence organisms shall be further described in the call Sequence if "n," "Xaa," or a modified base was used in a sequence; if "n," "Xaa," or "Inknown"; if molecule is combined DNA/RNA.  Call Sequence organisms shall be further described in the call Sequence if "n," "Xaa," or a modified base was used in a sequence; if "n," "Xaa," or indication, the "Danish Sequence organisms shall be further described in the call Sequence if "n," "Xaa," or a modified base was used in a sequence call Sequence if "n," "Xaa," or a modified base was used in a sequence call Sequence if "n," "Xaa," or a modified base was used in a sequence call Sequence if "n," "Xaa," or a modified base was used in a sequence call Sequence if "n," "Xaa," or a modified base was used in a sequence call Se			sequence con-	
ments, the type shall be "DNA." In ad- dition, the combined DNA/ RNA molecule shall be further described in the <220 to <223> feature section. <pre> </pre> <pre> </pre> <pre> </pre> <pre> <pre> </pre> <pre> </pre> <pre> <pre> <pre> <pre> </pre> <pre> <pre> <pre> <pre> <pre> </pre> <pre> </pre> <pre> <pre> </pre> <pre> <pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre>	•		tains both DNA	
type shall be "DNA." In addition, the combined DNA/ RNA molecule shall be further described in the <220> to <223> feature section.  C213> Organism Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.  C220> Feature Leave blank after c220> to <223> feature section.  C220> Feature Leave blank after described in the c320> to <223> feature section.  C220> Feature Leave blank after description of points of bio- logical signi- ficance in the sequence.  C221> Name/Key Provide appropriate identifier for feature, pre- ferably from MIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6  C222> Location Specify location Within sequence;  M, under the fol- lowing conditions: if "n," "Xaa," or a modified or modified or unusual L-amino acid or if molecule is combined DNA/RNA.  M, under the fol- lowing conditions: if "n," "Xaa," or a modified or a sequence  C222> Location Specify location within sequence;  M, under the classing the further described in the c220> c221> M, under the combined DNA/RNA.  M, under the fol- lowing conditions: if "n," "Xaa," or a modified or a modifi			<del>-</del>	
"DNA." In addition, the combined DNA/ RNA molecule shall be further described in the <220> to <223> feature section.  <213> Organism Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.  <220> Feature Leave blank after <220> <221-223> feature section.  <220> Feature Leave blank after <220> <221-223> feature section.  <220> Feature Provide for a description of points of biological significance in the sequence. If modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.  <221> Name/Key Provide appropriate identifier for feature, prefeature, prefeatu				
dition, the combined DNA/ RNA molecule shall be further described in the <220> to <223> feature section.    Combined DNA/ RNA molecule shall be further described in the <220> to <223> feature section.    Combined DNA/ RNA molecule shall be further described in the <220> to <221> feature section.    Combined DNA/ RNA molecule shall be further described in the <220> to <223> feature section.    Combined DNA/   Co				
combined DNA/ RNA molecule shall be further described in the <220> to <223> feature section. <pre> </pre> <pre> </pre> <pre> <pre> </pre> <pre> <pre> </pre> <pre> <pre> <pre></pre></pre></pre></pre></pre>		•		
RNA molecule shall be further described in the <220> to <223> feature section.    Call   Call   Call				
shall be further described in the <220> to <223> feature section.    Commonstrate				
described in the <220> to <223> feature section.  <213> Organism Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature Section.  <220> Feature Leave blank after <220> <221-223> following conditions: if "n," description of points of biological significance in the sequence.    Value   Valu		·		
<pre>&lt;223&gt; feature</pre>				···
Section.    Scientific name, i.e. Genus/species, Unknown or Artificial SequenceIn addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220 to <223 feature section.			the <220> to	
Scientific name, i.e. Genus/species, Unknown or Artificial SequenceIn addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	•	•	<223> feature	
i.e. Genus/species, Unknown or Artifi- cial Sequence In addition, the "Unknown" or "Artificial Se- quence" organisms shall be further described in the <220> to <223> feature section. <pre> </pre> <pre> <a href="#">&lt;220&gt;</a> (221-223&gt; following condi- provide for a description of points of bio- logical signi- ficance in the sequence.  In addition, the "Unknown" or description of provide for a description of points of bio- logical signi- ficance in the sequence.  In addition, the "Unknown or "Xaa," or a modi- ified or unusual logical signi- cial Sequence or "Unknown"; if molecule is combined DNA/RNA.  </pre> <a href="#">&lt;221&gt;</a> Name/Key Provide appropriate identifier for feature, pre- ferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6 asequence;  Specify location W, under the fol- lowing conditions: a modified or a modified or a modified or base was used in a sequence.  % Appendix 2, Tables 5 and 6 a sequence.  W, under the fol- lowing conditions: for modified base was used in a sequence.  % Appendix 2, Tables 5 and 6 graphical for within sequence; for modified or have described in the "Unknown"; for modified or a modified or base was used in a sequence.  % Appendix 2, Tables 5 and 6 graphical for gr		•	section.	
i.e. Genus/species, Unknown or Artifi- cial Sequence In addition, the "Unknown" or "Artificial Se- quence" organisms shall be further described in the <220> to <223> feature section. <pre> </pre> <pre> <a href="#">&lt;220&gt;</a> (221-223&gt; following condi- provide for a description of points of bio- logical signi- ficance in the sequence.  In addition, the "Unknown" or description of provide for a description of points of bio- logical signi- ficance in the sequence.  In addition, the "Unknown or "Xaa," or a modi- ified or unusual logical signi- cial Sequence or "Unknown"; if molecule is combined DNA/RNA.  </pre> <a href="#">&lt;221&gt;</a> Name/Key Provide appropriate identifier for feature, pre- ferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6 asequence;  Specify location W, under the fol- lowing conditions: a modified or a modified or a modified or base was used in a sequence.  % Appendix 2, Tables 5 and 6 a sequence.  W, under the fol- lowing conditions: for modified base was used in a sequence.  % Appendix 2, Tables 5 and 6 graphical for within sequence; for modified or have described in the "Unknown"; for modified or a modified or base was used in a sequence.  % Appendix 2, Tables 5 and 6 graphical for gr				
Unknown or Artificial Sequence In addition, the "Unknown" or "Artificial Sequence organisms shall be further described in the <220> to <223> feature section. <pre> &lt;220&gt; Feature</pre>	<213>	Organism		M
cial SequenceIn addition, the "Unknown" or "Artificial Se- quence" organisms shall be further described in the <220> to <223> feature section.  <220> Feature  Leave blank after <220> <221-223> following condi- tions: if "n," description of points of bio- logical signi- logical signi- ficance in the sequence.  Provide appropriate identifier for identifier for feature, pre- ferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6  Specify location W, under the fol- lowing conditions: if "n," "Xaa," or a modified base was used in molecule is combined DNA/RNA.  M, under the fol- lowing conditions: if "n," "Xaa," or a modified or un usual L-amino acid or modified base was used in a modified or un usual L-amino acid or modified base was used in a modified or un usual L-amino acid or modified base was used in a sequence:  M, under the fol- lowing conditions: if "n," "Xaa," or a modified or un usual L-amino acid or modified base was used in a sequence:  M, under the fol- lowing conditions: if "n," "Xaa," or a modified or un usual L-amino acid or modified base was used in a sequence:  M, under the fol- lowing conditions:			<del>-</del>	
addition, the "Unknown" or "Artificial Se- quence" organisms shall be further described in the <220> to <223> feature section.  <			,	
"Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.   Carried for a description of points of bio- logical signi- ficance in the sequence.  Call Name/Key  Provide appropriate identifier for feature, pre- feature, pre- feature, pre- feature, pre- ferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6  "Unknown" M, under the fol- lowing conditions: for "Xaa," or a mod- points of bio- ified or unusual L-amino acid or modified base was used in a se- quence; if ORGAN- ISM is "Artifi- cial Sequence" or "Unknown"; if molecule is combined DNA/RNA.  Call Name/Key  Provide appropriate if "n," "Xaa," or a modified or un- usual L-amino acid or modified base was used in a sequence  Appendix 2, base was used in a sequence  M, under the fol- lowing conditions: for "n," "Xaa," or a modified or un- usual L-amino acid or modified base was used in a sequence  Call Name/Key  Provide appropriate if "n," "Xaa," or a modified or un- usual L-amino acid or modified base was used in a sequence  Call Name/Key  Provide appropriate if "n," "Xaa," or a modified or un- usual L-amino acid or modified base was used in a sequence  Call Name/Key  Provide appropriate if "n," "Xaa," or a modified or un- usual L-amino acid or modified base was used in a sequence	•	• •		
"Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.    Combined provide for a description of points of biological significance in the sequence.	·			
quence" organisms shall be further described in the <220> to <223> feature section. <pre> </pre> <pre> <pre> <pre> </pre> <pre> <pre> <pre> <pre></pre></pre></pre></pre></pre></pre>				
shall be further described in the <220> to <223> feature section.    Comparison   C				-
<pre></pre>				
feature section.    Comparison			described in the	
Combined DNA/RNA.   Comb			<220> to <223>	
<pre></pre>			feature section.	_
<pre></pre>	<2205	Factores	Tarana halaman finan	M
provide for a description of points of bio- ified or unusual logical signi- L-amino acid or ficance in the sequence.    Value		reature		•
description of points of bio- logical signi- ficance in the modified base was used in a sequence; if ORGAN- ISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.  C221> Name/Key Provide appropriate identifier for lowing conditions: feature, pre- ferably from a modified or un- WIPO Standard usual L-amino ST.25 (1998), acid or modified Appendix 2, base was used in a sequence  C222> Location Specify location M, under the fol- within sequence; within sequence;  M, under the fol- lowing conditions: M, under the fol- lowing conditions:	Trape pro many ug			_
points of bio- logical signi- ficance in the modified base was used in a se- quence; if ORGAN- ISM is "Artifi- cial Sequence" or "Unknown"; if molecule is combined DNA/RNA.   Provide appropriate M, under the fol- identifier for lowing conditions: feature, pre- if "n," "Xaa," or ferably from a modified or un- WIPO Standard usual L-amino ST.25 (1998), acid or modified Appendix 2, base was used in Tables 5 and 6  Apecify location M, under the fol- within sequence; lowing conditions:			•	
logical significance in the sequence.  In the sequence in the sequence, if ORGAN-ISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.  In the sequence of the sequence				
sequence.  sequence:  used in a sequence; if ORGAN-ISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.  Provide appropriate  identifier for lowing conditions:  feature, pre- ferably from a modified or un- WIPO Standard usual L-amino ST.25 (1998), acid or modified Appendix 2, base was used in a sequence  Location Specify location M, under the fol- within sequence;  Wied in a sequence in ORGAN-ISM is PRORGAN-ISM is				L-amino acid or
quence; if ORGAN- ISM is "Artifi- cial Sequence" or "Unknown"; if molecule is combined DNA/RNA. <pre> </pre> <pre> </pre>			ficance in the	
ISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.    Name/Key   Provide appropriate   M, under the folidentifier for lowing conditions: feature, prefeature, preferably from a modified or unWIPO Standard usual L-amino ST.25 (1998), acid or modified happendix 2, Tables 5 and 6 a sequence			sequence.	
cial Sequence" or "Unknown"; if molecule is combined DNA/RNA.  <221> Name/Key Provide appropriate M, under the fol- identifier for lowing conditions: feature, pre- if "n," "Xaa," or ferably from a modified or un- WIPO Standard usual L-amino ST.25 (1998), acid or modified Appendix 2, base was used in Tables 5 and 6 a sequence  <222> Location Specify location M, under the fol- within sequence; lowing conditions:				
"Unknown"; if molecule is combined DNA/RNA.  <221> Name/Key Provide appropriate M, under the folidentifier for lowing conditions: feature, pre- if "n," "Xaa," or ferably from a modified or un-WIPO Standard usual L-amino ST.25 (1998), acid or modified Appendix 2, base was used in Tables 5 and 6 a sequence  <222> Location Specify location M, under the folwithin sequence; lowing conditions:				
<pre>Molecule is combined DNA/RNA.  &lt;221&gt; Name/Key Provide appropriate M, under the fol- identifier for lowing conditions:     feature, pre-     if "n," "Xaa," or     ferably from a modified or un- WIPO Standard usual L-amino _ ST.25 (1998), acid or modified Appendix 2, base was used in Tables 5 and 6 a sequence  &lt;222&gt; Location Specify location M, under the fol- within sequence; lowing conditions:</pre>		•		
<pre>Combined DNA/RNA.  Combined DNA/RNA.  Reprovide appropriate M, under the folidentifier for lowing conditions:</pre>				
<pre>Name/Key Provide appropriate M, under the fol- identifier for lowing conditions:     feature, pre-     if "n," "Xaa," or     ferably from a modified or un- WIPO Standard usual L-amino _ ST.25 (1998), acid or modified Appendix 2, base was used in Tables 5 and 6 a sequence</pre> <pre>&lt;222&gt; Location Specify location M, under the fol- within sequence; lowing conditions:</pre>				
identifier for lowing conditions: feature, pre- if "n," "Xaa," or ferably from a modified or un- WIPO Standard usual L-amino ST.25 (1998), acid or modified Appendix 2, base was used in Tables 5 and 6 a sequence  <222> Location Specify location M, under the fol- within sequence; lowing conditions:	•			combined by A MA.
identifier for lowing conditions: feature, pre- if "n," "Xaa," or ferably from a modified or un- WIPO Standard usual L-amino ST.25 (1998), acid or modified Appendix 2, base was used in Tables 5 and 6 a sequence  <222> Location Specify location M, under the fol- within sequence; lowing conditions:	<221>	Name/Key	Provide appropriate	M, under the fol-
ferably from a modified or un- WIPO Standard usual L-amino _ ST.25 (1998), acid or modified Appendix 2, base was used in Tables 5 and 6 a sequence  <222> Location Specify location M, under the fol- within sequence; lowing conditions:	N		identifier for	lowing conditions:
WIPO Standard usual L-amino _ ST.25 (1998), acid or modified Appendix 2, base was used in Tables 5 and 6 a sequence  <222> Location Specify location M, under the fol- within sequence; lowing conditions:				
ST.25 (1998), acid or modified Appendix 2, base was used in Tables 5 and 6 a sequence  <222> Location Specify location M, under the fol- within sequence; lowing conditions:				
Appendix 2, base was used in Tables 5 and 6 a sequence  <222> Location Specify location M, under the folwithin sequence; lowing conditions:				<del>-</del>
Tables 5 and 6 a sequence  <222> Location Specify location M, under the fol- within sequence; lowing conditions:				·
<pre>&lt;222&gt; Location Specify location M, under the fol- within sequence; lowing conditions:</pre>				
within sequence; lowing conditions:			rables 5 and 6	a sequence
within sequence; lowing conditions:	<222>	Location	Specify location	M, under the fol-
		•		
			where appropriate	if "n," "Xaa," or
state number of a modified or un-				
first and last usual L-amino		•		
bases/amino acids acid or modified			bases/amino acids	acid or modified

		in feature	base was used in a sequence
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial
	. \	-	Sequence" or "Unknown"; if molecule is com-
MARIE PARAMETER	* . * ***	•	bined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	0
<301>	Authors	Preferably max of ten named authors of publi- cation; specify one name per line; preferable format: Surname, Other Names and/or Initials	
<302>	Title		0 ;
<303>	Journal	•	0
<304>	Volume	<del>.</del> ,	0
<305>	Issue		, o
<306>	Pages		0
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy	O .
<308>	Database Accession Number	Accession number assigned by data-base including database name	0
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy	0 -
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	O

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd	0
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	0
<313>	Relevant Residues	FROM (position) TO (position)	0
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence	М

- 5. Section 1.824 is revised to read as follows:
- 1.824 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.
- (a) The computer readable form required by 1.821(e) shall meet the following specifications:
- (1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.
- (2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.
- (3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.
- (4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.
- (5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.
- (6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.
- (b) Computer readable form submissions must meet these format requirements:
- (1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;
- (2) Operating System: MS-DOS, Unix or Macintosh;